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Outline of Microarray Chip Technology approach

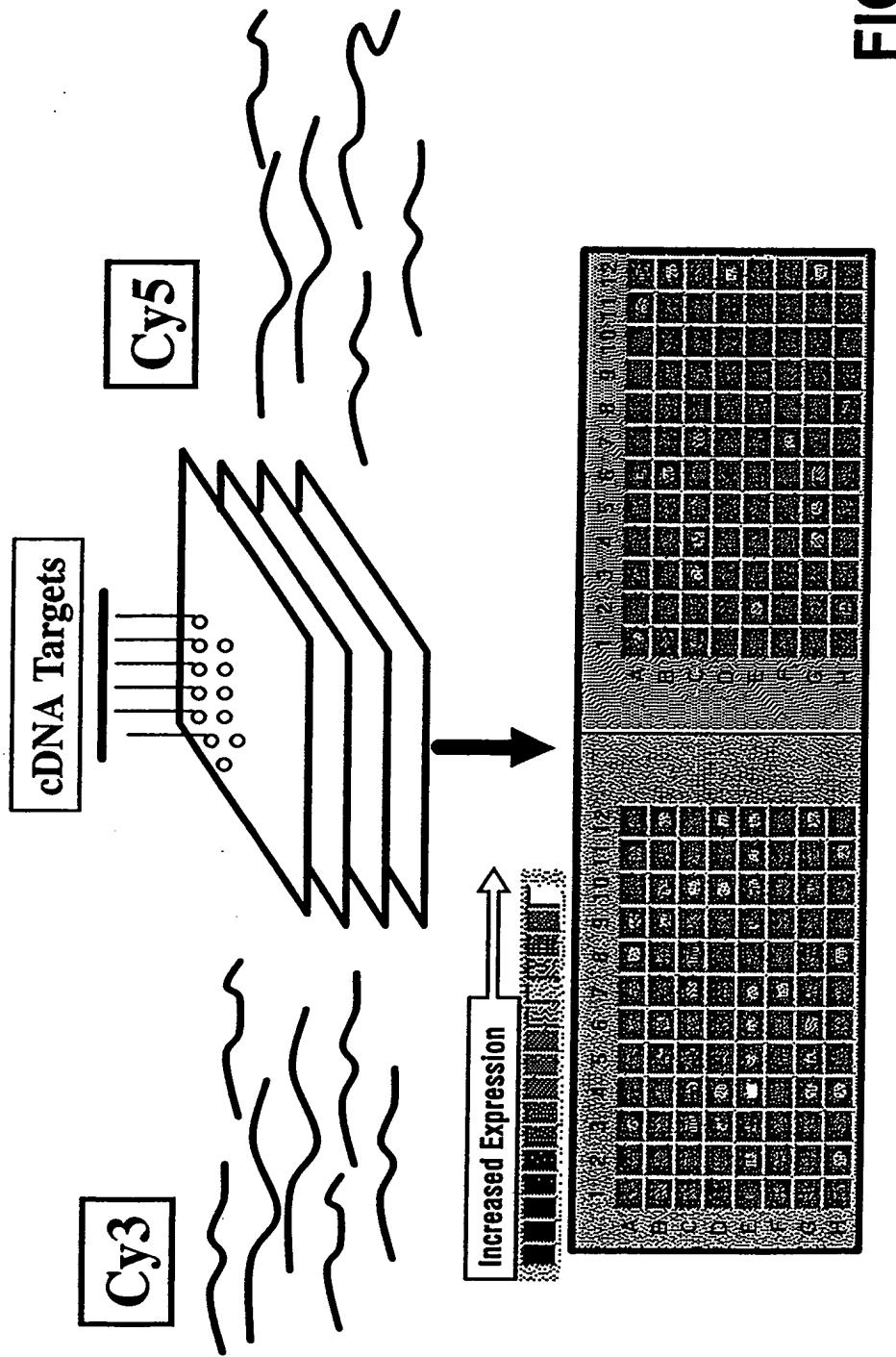
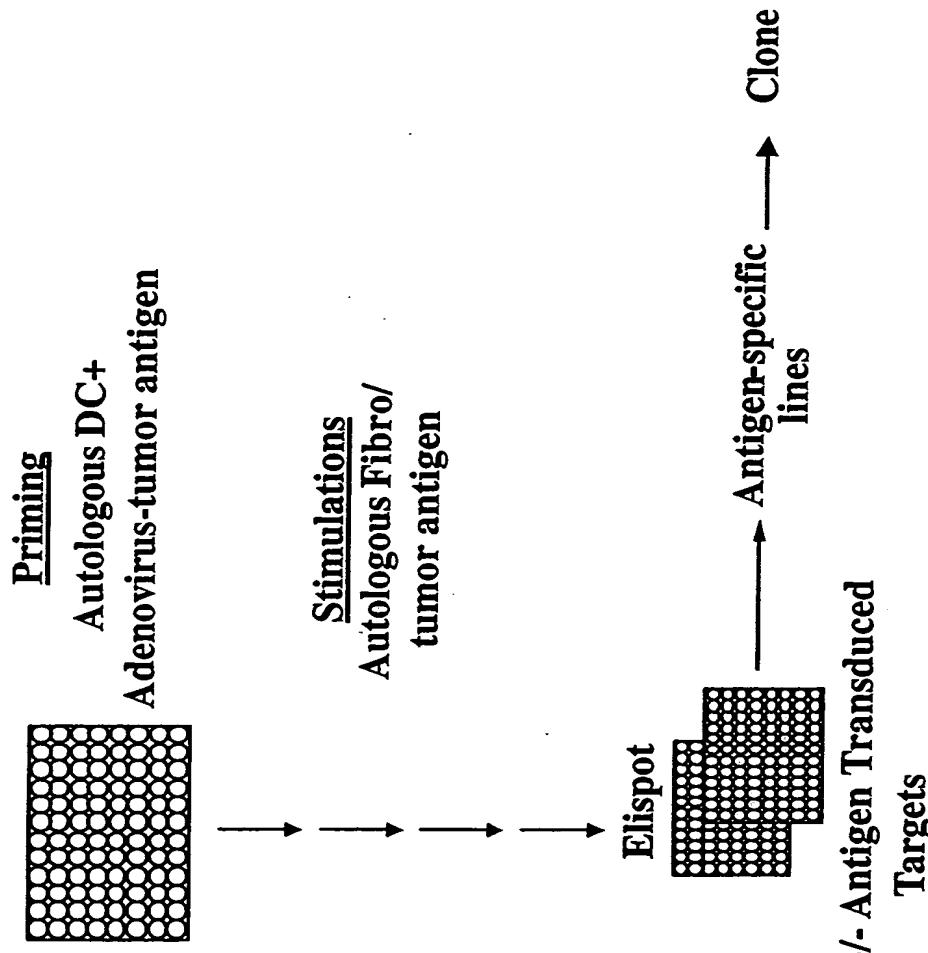


FIG. 1

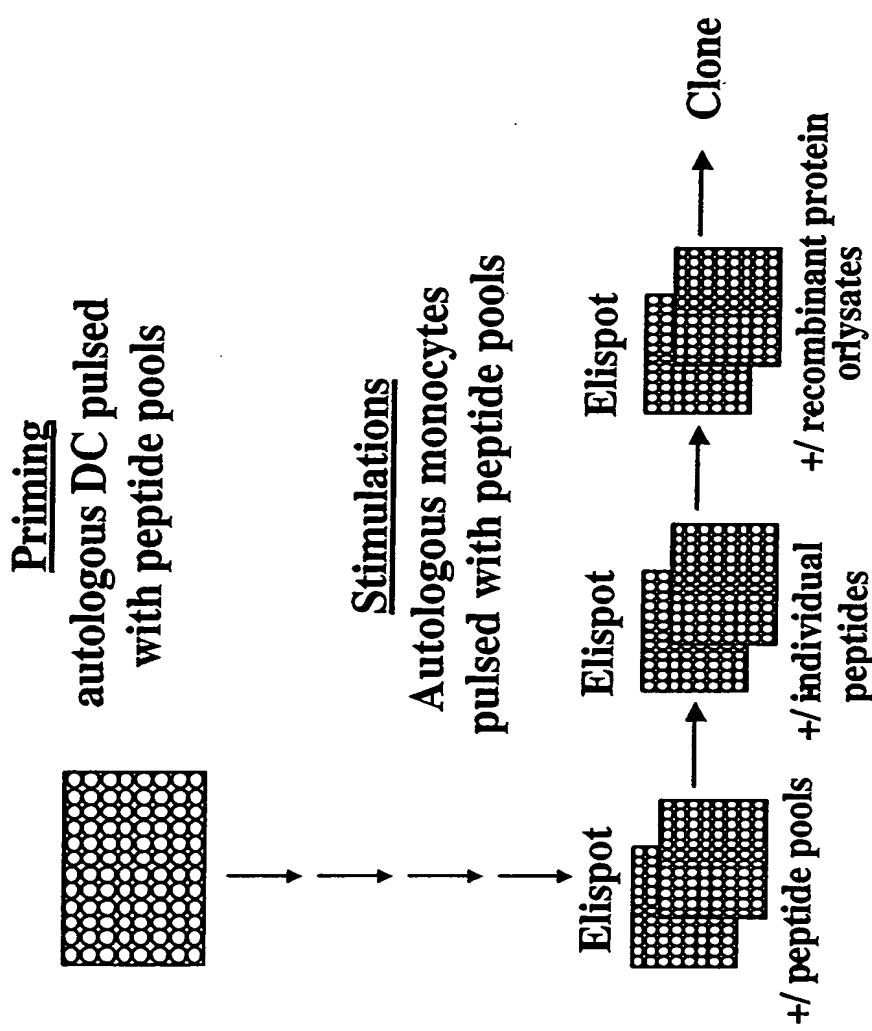
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General protocol for *in-vitro* whole gene CD8 T cell priming

**FIG. 2**

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General protocol for *in-vitro* whole gene CD4 T cell priming

**FIG. 3**

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LEUKEMIA/LYMPHOMA CHIP #3: PROBES USED IN ANALYSIS

Cy3 Probe		Cy5 Probe	
Tissue	RNA#	RNA#	Tissue
Lymphoma, T cell	952	SPACT74	Kidney N
Lymphoma, B cell	955	SPACT81	Liver N
Lymphoma, B cell	953	SPACT78	Lung N
Lymphoma	916	SPACT42	Brain N
Lymphoma, Hodgkins	950	138598B	Skin N
Lymphoma, Hodgkins	950	SPACT49	Bone Marrow N
Lymphoma, B cell	CL151	888	PBMC resting
Lymphoma, T cell	904B	SPACT55	Stomach N
Lymphoma, Hodgkins see RNA 959	CL153	SPACT70	Thymus N
Lymphoma, B cell	CL152	SPACT75	Skeletal Muscle N
Lymphoma, B cell see RNA 958	CL155	SPACT73	Heart N
Lymphoma, B cell	944	243502B	Esophagus N
Lymphoma, B cell	958	1006	Colon N
Lymphoma, B cell	954	SPACT65	Small Intestine N
Lymphoma	960	779B	Trachea N
Lymphoma, T cell	957	S9327328	Bladder N
Lymphoma, B cell	914B		
Lymphoma, B cell	913		
Lymphoma, B cell	944B		
Lymphoma, B cell/failed	903		

GREEN: Tumor probes where gene expression would be desired.

RED: Normal essential tissue probes where gene expression is to be avoided.

BLACK: Normal tissue probes where gene expression is acceptable.

FIG. 4

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Hematology Therapeutic Ab Candidates

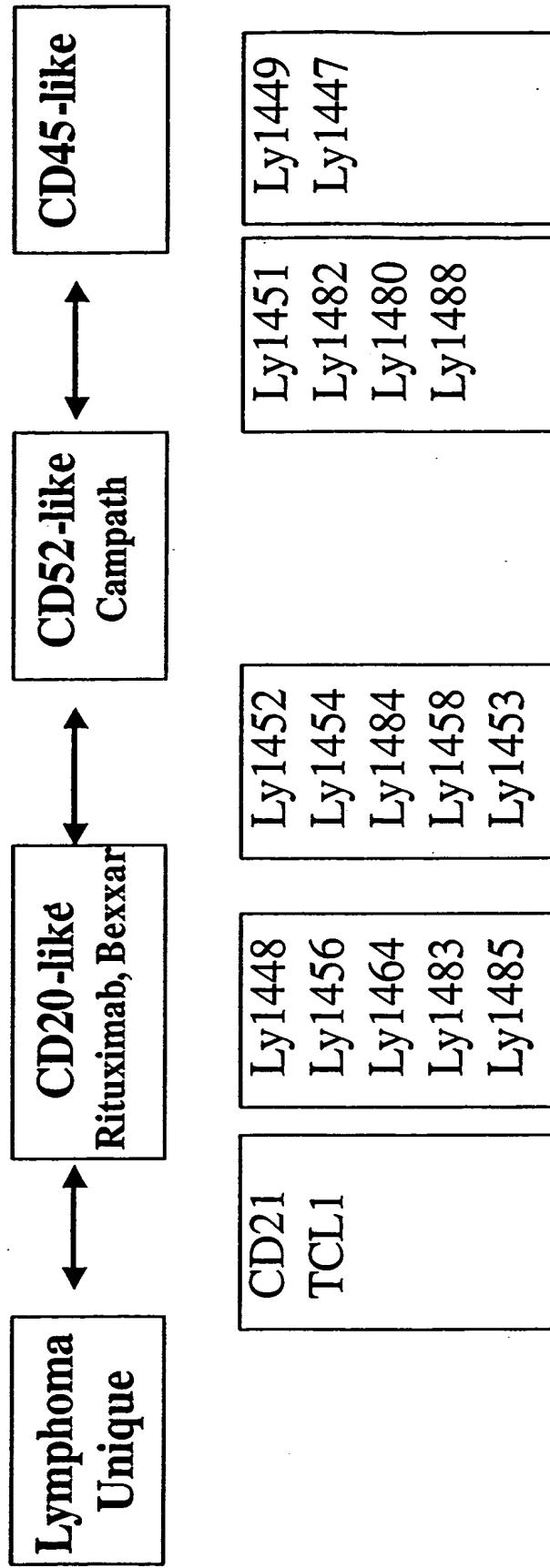


FIG. 5

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a. TMpred Report for Ly1484 Long

RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAAPSLANISCF
 TQKLVEKLYSGMFADPRHILLFILEHIMVVIE TASSQRTDVLSTLYSSL
 NKVILYCLSKPQOSLSECILGLSILCFLQEHWDVVVFAT YNSNISFLLCLM
 HCLLLNERSYPEFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDV
 QHNIQKTVQTLWQQLVAQRQQTLEDAFKIDLSPKGEREVKIEEVTPLWE
 ETMLKAWQHYLASEKKSLASRSNVAAHSKVTLWSGSLSAMKLMPGRQAK
 DPECKTEDFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQ
 EQLFGEGLWSQGEETKPCSPWELDWREGPARMRKRIKRLSPLAESSGR
 HKESQDKNDHISQTNAENQDELTREAEGEDEVGVDCQLTFFPALHES
 LHSEDFLELCRERQVILQELLDKEKVTQKFSLVIVQHLSSECVLLFGHQ
 HFVTCENFTLSPTCDVYCTRHCLSNISDPPFIFNLCSKDRSEDHYSQOCHS
 YADMRELROARFLLQDIALEIFFHNGYSKFLV FYNNDRSKAFKSFCSFQP
 SLKGKATSEDTLNLRYPGSDRIMLQWKQKRDISNFEYLMYLNTAAGRTC
 NDYMQYPVFPWVLADYTSETLNLANPKIFRDLSKPMGAQTKERKLKFIQR
 FKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPFTQAFCALQCGSFD
 VADRMFHVKSTWESASRENMSDVRELTPEFFYLPEFLNCNGVEFGCMQ
 DGTIVLGDVQJLPPWADGDPRKFISLHRKALESDFVSANLHHWIDLIFCYKQ
 QCPAAVDAVNIFHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKOLF
 TKPHPARTAACKPLPGKDVTSPVSLPCHPOPFFYSLOSLRPSQVTVKDMY
 LFSLGSESPKGATCHIVSTEKPTILLAVERNKVLLPPLWNRTFSWGFDDFSC
 CLESYGSDKVLMFENLAACRCLCAVCPSPTRIVTSCTSTVVVCWELSM
 TKGRPRGLRLRQALYCHTOAVTCLAASVTFSLLVSCSODCTCTILWDLDHL
 THVTRLPAHREGISATTISDVSGTIVSCAGAHLSLWNVNQPLASITTAW
 GPEGAITCCCLMECPAWDTSOTIITGSQDGMRVWKTEDVKMSVPGRPAG
 EEPLAQOPPSPRGHKWEKNLALSRELDVSTALTGKPSKTSPAVTALAVSRN
 HTKLIVGDERGRIFCWSADG (SEQ ID NO: 120)

Black = INTRACELLULAR, Red = TRANSMEMBRANE,
 Blue = EXTRACELLULAR

Ly1484 Long has 1269 amino acids and 5
 Transmembrane Domains

Transmembrane Domain 1: 63 - 84	Score: 1.36675
Transmembrane Domain 2: 118 - 139	Score: 1.38695
Transmembrane Domain 3: 480 - 501	Score: 1.36185
Transmembrane Domain 4: 562 - 583	Score: 1.31785
Transmembrane Domain 5: 725 - 746	Score: 1.3521

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b. TMpred Report for Ly1484 (short)

MLQKWQKRDISNFEYLMYLNTAAGRTCNDYMQYPVFPWVLADYTSETLNL
ANPKIFRDL SKPMGAQTKERKLFIQRFKEVEKTEGDMTVQCHYYTHYSS
AIIVASYLVRMPPFTQAFCALQCCSF DVA DRM FHSVKSEWESASRENMSD
VRELTPEFFYLPEFLTNCNGVEFCCMODGTVLGDVOLPPWADCDPRKFIS
LHRKALESDFVSA NLHHWIDLIFCYKQOQPAAVDAVNTFHPYFYGDRMDL
SSITDPLIKSTI LCFVSNFCQVPKOLFTKPHPARTAAGKPLPCKDVSTPV
SLPGHPQPFYSLQSLRPSQVTVKDMYLFLSGSESPKGAIHVSTEKT
LAVERNKVLLPPLWNRTFSWGFDDFSCCLGSYGS DKVLMTFENLAAWGR
LCAVCPSPTTIVTSGISTVVVCVWE LSMTKGRPRCLRLRQALYCHTOAVTC
LAASVTFSLLVSGSQDCTCILWDL DHLTHVTRLPAHREGTSAITISDVSG
TIVSCACAHLSLWNVNNGOPLASITTAWGP EGAITCCCLMECPAWDTISQII
TIGSQDGIVRVWKTEDVKMSVPGRPAGEEPLAOPPSPRGHKWEKNLALSR
ELDVSTALTGKPSKTPSPAVTALAVSRNHTKLLVGDERGRIFCWSADG

(SEQ ID NO: 121)

Black = INTRACELLULAR, Red = TRANSMEMBRANE,

Blue = EXTRACELLULAR

Ly1484 has 646 amino acids and 1 Transmembrane
Domains

Transmembrane Domain 1: 102 - 123 Score: 1.3521

FIG. 6 (cont.)

ANALYSIS RESULTS OF THE PROGRAM TSITES.

These are the results of the analysis of the file--> LY1484~1.TXT
Beginning with residue: 1 and ending with residue: 1270
AMPHI Window size: 11

A-AMPHI mid points of blocks.
 R-Residues matching the Rothbard/Taylor motif.
 D-Residues matching the IAD motif.
 Q-Residues matching the IED motif.

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FIG. 7

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155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
HCLLILNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDILPSLSDVQHNIQKTVQTLWQQQLVAQRQQTLED
.....AAAAA.AAAAAAA.....
.....RRRR.....R.....

230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
AFKIDLSVKPGEREVKIEEVTPLWEITMLKAWQHYLASEKKSLSRSNVAHHHSKVTLWSGSLSSAMKLMPGRQAK
.....AAAA...AAAAA.....
.....RRRRRRRRRRRRR.....
.....
.....ddda.....

305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
DPECKTEDFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQEQLFGELGLWSQGEETKPCSPWELD
.....AAAAA...AAAAA.....AAAAA.....AAAAA.....
.....RRRR.....RRRRR.....RRRR.....
.....

380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
WREGPARMRKRKRLSPLEALSSGRHKE\$QDKNDHISQTNAENQDELTIREAEGEPDEVGVDC\$QLTFFPALHES
.....AAAAA.....AAAAA.....
.....RRRR.....DDDDDD.....
.....dddd.....

FIG. 7 (cont.)

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FIG. 7 (cont.)

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FIG. 7 (cont.)

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FIG. 7 (cont.)

ANALYSIS RESULTS OF THE PROGRAM ISITES.

These are the results of the analysis of the file--> LY1484~2.TXT
Beginning with residue: 1 and ending with residue: 647
AMPHI Window size: 11

A-AMPHI mid points of blocks.
 R-Residues matching the Rothbard/Taylor motif.
 D-Residues matching the IAD motif.
 d-Residues matching the IED motif.

(SEQ ID NO: 121)

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FIG. 8 (cont.)

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530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
AWGPEGAITCCCLMEGPAWDTSQIITGSDGMVRVWKTEDVKMSVPGRPAGEEPLAQOPPSPRGHKWEKVNLA
S...
A.....AAAAAA
R.....RRRRRR
D.....DDDDDD
.....
605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
ELDVSIALTGKPSKTSAPAIVTALAVSRNHTKLLVGERGRIFCW
SADG
.....
D.....DDDDDD
.....
d.....ddddd
.....

FIG. 8 (cont.)

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